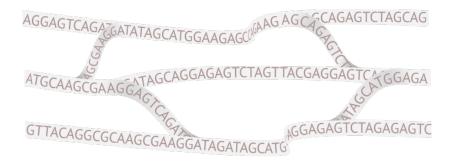
COMPUTING OPTIMAL FLOW DECOMPOSITIONS FOR ASSEMBLY

Kyle Kloster, **Philipp Kuinke**, Michael P. O'Brien, Felix Reidl, Fernando Sánchez Villaamil, Blair D. Sullivan, Andrew van der Poel

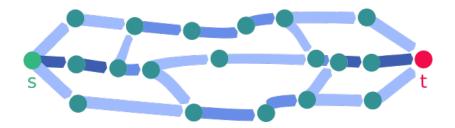
2018/03/27

North Carolina State University RWTH Aachen University

MOTIVATION

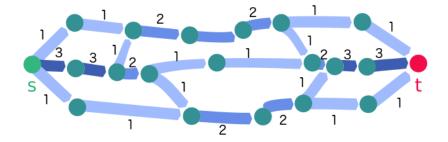


Shared segments between DNA/RNA strands create ambiguity in the assembly problem



Connecting overlapping segments and counting their frequencies yields a splice-graph.

The Problem





The problem is to split the flow into *s*-*t*-paths, to recover the original DNA/RNA strands.

The Problem



AGGACGTAGATAGCTAGCTAATGCTACGATCAGAGGACGTAGATTTATTACCAT TACCGAATACGAACTAGGATATCGATCGATCGAGAGGCCCAATAGGGAATATCCG TACCGAATACGAACTAGGATATCGATCGATTGATCT ATAATAGTAGAATATCCG AGGACGTAGATAGCTAGCTAATGCTACGATCAGAGGACGTAGATTTATTACCAT TACCGAATACGAACTAGGATATCGATCGATCAGAGGCCCAATAGGGAATATCCG

The Problem



- k-Flow Decomposition (k-FD)

- *Input:* (G, f, k) with an *s*-*t*-DAG *G*, a flow *f* on *G*, and a positive integer *k*.
- *Problem:* Find an integral *flow decomposition* of (G, f) using at most k paths.

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M. Shao & C. Kingsford

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Problem is NP-hard even for weights {1, 2, 4}

How to split a flow? T. Hartman et. al. About ten years ago, some computer scientists came by and said they heard we have some really cool problems. They showed that the problems are NP-complete and went away!

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linear fpt: exponential only in the *parameter* and linear in *n*!

Data used by Shao and Kingsford:

- 1. 99% of instances decompose into ≤ 8 paths. → exploit **small natural parameter**.
- 2. ~4 million mostly small instances.
 - \rightarrow handle **large throughput**.
- 3. Output decompositions.
 - \rightarrow reliably recover **domain-specific solution**.

Toboggan solves k-FD in $2^{O(k^2)}(n + \lambda)$, where λ is the logarithm of the largest flow value.

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- Run-time competitive with current state of the art heuristic
- Usable in practice

IMPLEMENTATION & EXPERIMENTS



https://github.com/theoryinpractice/toboggan

Dataset: Available from Shao and Kingsford. Simulated sequencing data for human, mouse and zebrafish, containing ground-truth. Dataset: Available from Shao and Kingsford. Simulated sequencing data for human, mouse and zebrafish, containing ground-truth.

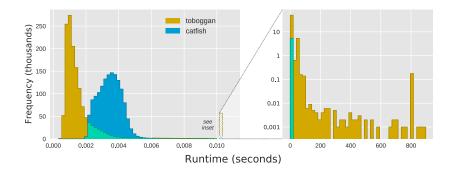
> Deviation from original setup: Trivial instances omitted. Removes around 64% of the 4M graphs.

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Dedicated system with Intel i7-3770: 3.40 GHz, 8 MB cache and 32 GB RAM.

Execution Time



Median:

Toboggan: 1.24ms

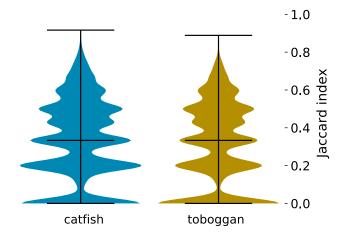
Catfish: 3.47ms

dataset	instances	minimal	non-minimal
zebrafish	445,880	99.907%	0.053%
mouse	473,185	99.401%	0.074%
human	529,523	99.490%	0.043%
all	1,448,588	99.589%	0.056%

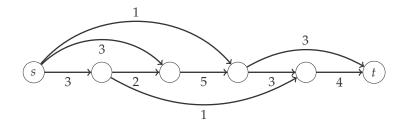
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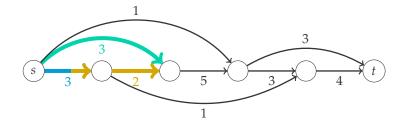
k	instances	Catfish	Toboggan
2	63.2791%	0.992	0.995
3	22. 0775%	0.967	0.969
4	8.5237%	0.931	0.930
5	3.4920%	0.886	0.886
6	1.5375%	0.830	0.828
7	0.6698%	0.788	0.780
8	0.2889%	0.767	0.766
9	0.1241%	0.740	0.743
10	0.0070%	0.752	0.802
11	0.0004%	0.500	0.500
all	100%	0.973	0.975

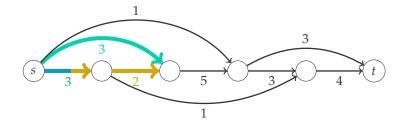
Solutions vs. Ground Truth



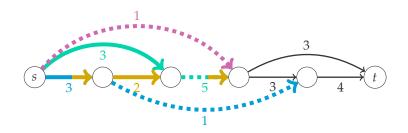
ALGORITHM IDEA



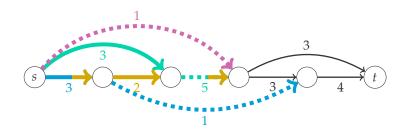




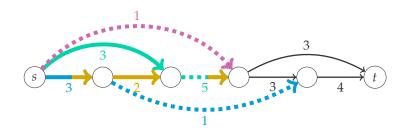
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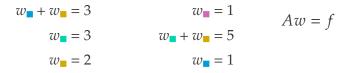


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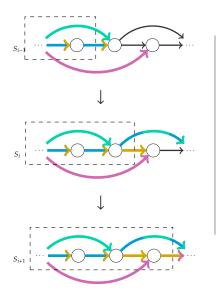




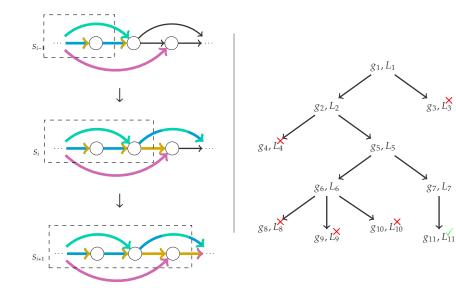




Dynamic Programming



Dynamic Programming





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paper: https://arxiv.org/abs/1706.07851

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Thank you!

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